

FIGURE 1B

1201 CATCCTGTGT ATATCGTGCA GGATGGGCC CCCAGAGCC CTCCAACAT CTACTACACA TCGATTTCTG TGTGGAGTG GCCATATTG CATACGATAC
 GTAGGACACA TATAGCACGT CCTACCCGG GGGTCTCGG GAGTTTGTG GATGATGTG AGCTAAAGAC ACAACCTCAC CGGTATAAC GTATGCTATG
 320 HisProValT yrIleValG1 nAspGlyPro ProGlnSerP roProAsnI1 eTyTyTrThr SerIleSerV alLeuGluTr pProIleLeu HisThrIleGln
 1301 AACTGTTTTT CATGCGATCC AAGTGCTCCC GTGTCACTAC ATTCCTTATT CTGTGCAAG TTATTACGAC ATCGACTTGC CGGATGACTT CATTTAGCTT
 TTGACAAAAA GTACGCTAGG TTCACGAGGG CACAGTGATG TAAGAATAAA GGACACGTTT AATAATGCTG TAGCTGAACG GCCTACTGAA GTAAATCGAA
 354 LeuPhePh eMetArgSer LysCysSerA rgValThrTh rPheLeuPhe ProValGlnV alIleThrTh rSerThrCys ArgMetThrS erPheSerPhe
 1401 TACCACCCTG AACCCATCCA TGCAGGCCTG CAGAGCACAG ATGGGGGAAT TCCGAATCAG ATGGTGTTC TGGGGGACA GGATCCTGGG TACGGCTCTG
 ATGGTGGGAC TTGGGTAGGT ACGTCCGGAC GTCTCGTGTG TACCCCTTA AGGCTTAGTC TACCACAAAAG ACCCCCCTGT CCTAGGACCC ATGCCGAGAC
 387 ThrThrLeu AsnProSerM etGlnAlaCy sArgAlaGln MetGlyGluP heArgIleAr gTrpCysPhe TrpGlyAspA rgIleLeuG1 yThrAlaLeu
 501 TTTGTGCTTG TGCTTATTCT TCTTCTTGGG AGGCTGAATA TGCATCAGAC GACACTGCTC CGGCAACGGG CCAGTGTGGA GGCGGAAGCC GGCCAGCATG
 AAACACGAAC ACGAATAAGA AGAAGAACCC TCCGACTTAT ACGTAGTCTG CTGTGACGAG GCCGTTGCCG GGTACACACCT CCGCTTCGG CCGGTCTGTAC
 420 PheValLeuV alLeuIleLe uLeuLeuGly ArgLeuAsnM etHisGlnTh rThrLeuLeu ArgGlnArgA laSerValG1 uAlaGluAla GlyGlnHisGly
 1601 GTCCCCCTGT ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG GAGGCTGCTG TTATCATGGG AACCAGGCAG ATCAATCATC
 CAGGGGACAC TATCCTAACT TTCTCGATGA CTCTTATCCC CCGAAGAGTT ACTCTCTCGC CTCCGACGAC AATAGTACCC TTGGTCCGTC TAGTTAGTAG
 454 ProLeu (SEQ ID NO: 2)
 1701 CCTGGCAGGT CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CTTTCTTCCC ACAGAAATTA TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTTCG
 GGACCGTCCA GTCCGTCTCT CAATGAATCG AAGAGGAAGT GGAAGAAGGG TGCTCTAAAT AATATCCGAA CAAGGTTCAA CATCACACAC TAGTCTAAGC
 1801 TGCTGCCTGT CAGCTCTGTG CTACCTGGCA GTTCCCTTCA GTTCCCTTCA TGAATTCGA TATCAAGCTT ATCGATACCG TCGACCT TCGACCT (SEQ ID NO: 1)
 ACGACGGACA GTCGAGACAC GATGGACCGT CAAGGGGAGT ACCTTAAGCT ATAGTTCGAA TAGCTATGGC AGCTGGA

FIGURE 2B

1101 GGAGGCTGAG CCCTGGGAGC TAGGGAATAGC TCTGGGGGT GCGGGCGCTG CAGATCCCCC CTCTGCCCC CACTATGAGA AGGTAGTGG TGACTATGGG
 287 CCTCCGACTC GGACCCCTCG ATCCCTATCG AGACGCCCA CGCCCCGAC GTCTAGGGG GAAGACGGG GTGATACCTT TCCACTCACC ACTGATACCC
 1201 GluAlaGlu ProGlyGluL euGlylleAl aLeuArgGly GlyGlyAlaA IaAspProPr oPheCysPro HisTyriGluL ysValserGI yAspTyriGly
 1201 CATCCCTGTG ATATCGTGCA GGATGGGCCC CCCCAGAGCC CTCCAAACAT CTACTACAAG GTATGAGGGC TCCCTCACC TGGCTATCCT GAATCCAGCC
 320 HisProValT ylleValGI nAspGlyPro ProGlnSerP roProAsnIl eTyTyriLys Valop* (SEA ID NO: 4)
 1301 GTTCTTGGG TGCTCCTCCA GTTTAATTC TGGTTTGAG GACACCTCTA ACATCTCGG CCCCAGCCCC CTTCACCTCT CCCGGCTGCT
 1401 GAAGAACCCC ACAGGAGGT CAAATTAAG ACCAACTCC CTCTGGAGA TGTAGAGCCG GGGGTCGGG GAACTGAGGA GGGCCGAGCA
 1401 GTCTCTGGCT CCACCTTTAG GATTCTTTAG GATTCCCACT GCCCCACTTC CTGCCCCCCC GTTTGGCCAT GTTTGGCCAT CTCTGTCTCA GTGTCCCTGG
 1501 CAGGAGCAGA GGTGMAANTC CTAAGGAATC CTAAGGGTGA CCGGGTGAAG GACGGGAGGG CAAACCGSTA CCCCACGGGG GAGACAGAGT CACAGGCAAC
 1501 ATCCTTTTTC CTGGGGAGG GGCACAGGCT CAGCTCTCTC TCTGACCATG ACCAGGCCAT CCTTGTCCCC CTTCACCCACC CAGAGCTAGG GCGGGGAACA
 TAGGAAAAAG GAACCCCTCC CCGTGTCCGA GTGGAGGAG AGACIGGTAC TGGTCCGTA GGAACAGGGG GAGTGGSTGG GTCTCGATCC CCGCCCTTGT
 1601 GCGGCTTTT TGGTGGCAC ACCAACCGTG GCGGAGGAGT GCGCTCTCTA CTGGTTTCT CTTCCTATTC TCTTATCTCT CCGTCTCTAG GTCTGTCTCT
 CGGTGGAAA CCGGCTTCTT GCGGAGGAGT GACCGAGAGT GACCGAGAGT GACCGAGAGT GACCGAGAGT GACCGAGAGT GACCGAGAGT GACCGAGAGT
 1701 CTTCCTTAGC ATCTCTCTCC CCACATCTCTC TTTCACCTCT TGGCTTCTT ATCTCTCTCT TCTTCTCTCT TCTTCTCTCT TCTTCTCTCT TCTTCTCTCT
 GAGGGGATCG TAGGAGGAGG GGTGTAGAGG AAGTGGGAG AAGTGGGAG AAGTGGGAG AAGTGGGAG AAGTGGGAG AAGTGGGAG AAGTGGGAG
 1801 CTTAGCTTTC AGCCCCCTT CTGACCTCTC ATACCAACCA CTCCCTCTAG TCTGCCAAA ATGGGGGCTT TACCCCGGA ATACCCCTCT CAGACTGTG AGGTGGGCTC
 GAAKCGAAG TCGGGGUGA GACTGGAGAG TATGGTGTGT GAGGGGAGT GAGGGGAGT GAGGGGAGT GAGGGGAGT GAGGGGAGT GAGGGGAGT
 1901 CTCAGGCCAT GGGCACCAG GCTCCATTCT CTGGCTTGGC CCAGGCTCT ACATCTTAC TCCAGCCATT TGGGGTGGT GGTCTATGAC AGCTACCATG
 GAGTCCGGTA CCGCTCGTCC CGAGTAAGA GACCGGACCG GGTCCGAGA TGTATGATG AGGTCCGTA ACCCCACCA CCGAGTACTG TCGATGGTAC
 2001 AGAGAGACTG TCCCGTTTTC TCCAGTGGCC AATAGCAAGA TATCAACCGG TCGGACATG TATGCACTG GTCTCATG CAGACTACGA CTTACCCCGT GAACCTTGGC
 TCTTCTTAC AGGGCAAAAC AGGTACCCCG TTAATCTTCT ATACTTGGC AGCCCTGTAC ATACCTGANC CAGACTACGA CTTACCCCGT GAACCTTGGC
 2101 GAAGTGAATT GCTCCAGACA AGAGGTGACC AGGCCCGGAC AGAAATGGC TGGGAAGTAG CAGAAGCAGT GCAGCAGGAA CTGGAAGTGC CTTCAATCCAG
 CTTCACTGAA CGAGGTCTGT TCTCCACTGG TCCGGGCTGT TCTTTACCGG ACCCTTCATC GTCTTCGTCA CGTCTCTCTT GACCTTCAAG GAACTAGCTC
 2201 GACAGGAAGT AGCACTTCTG AAACAGGAAG TGGTCTGGCT GGAACCTCAA GTGGCTTAGT CTGGGGGATC AGGAGGTGG AGGTGGATGG TCTTATTCTT
 CTGTCTCTCA TCGTGAAGAC TTTGTCTCTC ACCAGACCGA CCTTCAGGTT CACCGMATCA GACCCCTTAG TCCCTCCACC TCCACCTTACC AAGAAATAGA
 2301 GTGGAGAAGA AGGGGGGAA GAACCTCTCT TCAAGAGGAA CCTGGAACCTT ACTGACTGTA AGAGGTAGA GGTGGACCGA (SEA ID NO: 3)
 CACCTCTCT TCCCGGCTT CTTGAAGGAA AGTCTCTCTT CGACCTTGAA TCACTGACAT TCTCCATCT CCACCTGGCT

FIGURE 3A

AL-2b.L 1 5K T C T A G A A N T A G T G G A T C C C C C C G G G C T G C A G S A A T T C C G A C G S C C C C T

AL-2b.L 51 G G A A G G G C T C T G G T G G G G C T G A G C G C T C T G C C C C G G G G G G C C S S C A D A G

AL-2b.L 101 C A G G A A G C A G G T C C G C G T G G S C C C T G G G G C C A T C A G C T A C C S S G G T G G T C

AL-2b.L 151 C G G G C T G A A G A G C C A G G C A G G C A A G G C A G C C A C C C C S G G G G C T S S C C S A C

AL-2b.L 201 T T T G C G G G A G T T G G T G C C C C G C C C C C A G G G C T T G S C G G G G T C A T G G S G C

AL-2b.L 251 C C C C C C A T T C T G S G C C G G G G G G G T G C G A G T C G G G C C C T S C T G C T G C T

AL-2b.L 301 G G G G T T T T G G G G C T G G T G T C T G G G C T A G C C T G G A G C C T G T C T A C T G G A A

AL-2b.L 351 C T C G G C G A A T A A G A G G T T C C A G S C A G A G G G T G G T T A T C T G C T G T A C C C T C

AL-2b.L 401 A G A T C G G G G A C C S S C T A G A C C T S C T C T G C C C C G G G C C C G G G C C T C C T G C C

AL-2b.L 451 C C T C A C T C C T C T C C T A A T T A T G A G T T C T A C A A G C T G T A G C T G G T A G U G G G

AL-2b.L 501 T G C T C A G G G C C G T G T G A G G C A G C C C C T G C C C C A A A C C T C C T T G T C A

H10036 1 - - - - - G C C G A G G C T G T G A G G C A C C C C C T G C C C C A A A C C T C C T T G T C A

AL-2b.L 551 C T T G T G A T C G C C C A G A C C T G G A T C T C C G C T T C A C C A T C A A G T T C C A G G A G

H10036 43 C T T G T G A T C G C C C A G A C C T G G A T C T C C G C T T C A C C A T C A A G T T C C A G G A G

AL-2b.L 601 T A T A G C C C T A A T C T G T G G G C C C A G G A T T C C C C T C G C A C C A C G A T T A C T A

H10036 93 T A T A G C C C T A A T C T G T G G G C C C A G G A T T C C C C T C G C A C C A C G A T T A C T A

AL-2b.L 651 G A T C A T T G C C A C A T C G G A T S S A C C C G G G A G G G C C T G G A G A G C C T G C A G G

H10036 143 G A T C A T T C C C A C A T C G G A T S S A C C C G G G A G G G C C T G G G A G A G C C T G C A G G

AL-2b.L 701 G A G G T G T G T G C C T A A C C A G A G C A T G A A A G T G C T T C T C C G A G T G G G A C A A

H10036 193 G A A G T G T G T G C C T A A C C A G A G C A T G A A G T G C T T C T C C G A G T N G G A C A A

AL-2b.L 751 A G T C C C C G A G S A G G G G C T G T C C C C C G A A A A C C T G T G T C T G A A A T G C C A T

H10036 243 A G T C C C C G A G S A G G G G C T G T C C C C C G A A A A C C T G T G T C T G A A A T G C C A T

AL-2b.L 801 G G A A A G A G A C C G A G G G G C A G C C C A C A G C C T G G A G C C T G G G A A G G A G A A

H10036 293 G G A A A G A G A C C G A G G G G C A G C C C A C A G C C T G G A G C C T G G G A A G G A G A A

AL-2b.L 849 C C T G C C A G G T G A C C C C A C C A G C A A T G A A C C T C C C G G G T C C T G A A A G G

H10036 312 C C T G C C A G G T G A C C C C A C C A G C A A T G A A C C T C C C G G G T C C T G A A A G G

AL-2b.L 897 C C C C C T G C C C C T T C C C A G C A T G C C T G C A G T G G C T G G G C A G C A G G

H10036 352 C C C C C T G C C C C T T C C C A G C A T G C C T G C A G T G G C T G G G C A G C A G G

AL-2b.L 942 G G G G C - - - - T G G C G C T C C T T G C T G G G C G T G G G A G S S C C T G G S G G T S C C

H10036 442 G G G S N G T T T T G G C (SER 10 NO: 5)

AL-2b.L 998 A T G T G T T G C C G G A S A U G G G G S S C C A A G C C T T C G G A G A G T C G C C A C C C T G G

AL-2b.L 1038 T C C T G G C T C C T T C G S G A G G S A G G G T C T C T G G C C T S G G G G G T G S A G G T S

AL-2b.L 1088 G G A T G G G A C C T C G G C A G C C T G A S C C T G G C A G C T A G G G A T A G C T C T C C G C

AL-2b.L 1138 G C T G C S G G G C T G C A G A C C C C C C T T C T S C C C C A C A T A G A G A A G G T G A G

AL-2b.L 1139 TGGTGACTAT CATGCTGTGTATATCGTGCAGGATGGC JCCDECCAGA
 AL-2b.L 1233 GCGCTCGAAACATCTACTACAGATGGATTCTGTGTGTGGAGTGGCCCATTA
 AL-2b.L 1285 TTGGATACGATACAACTGTTTTCATGCCATCCAAAGTACTCCCGGTGTCAO
 AL-2b.L 1338 TACATTCTTATTTCCTGTGGAAGTTATTACGACATCGACTTGGCCGGATGA
 AL-2b.L 1388 CTTCATTTAGCTTTACCAAGCTGAACCCATCCATGCCAGGCGTGCAGAGCA
 AL-2b.L 1438 CAGATGGGGGAATTCCGAATCAGATGGTGTTCCTGGGGGGACAGGATCCT
 AL-2b.L 1486 GGGTACGGCTCTGTTTSTGCTTGTTGCTTATTCTTCTCTTGGGAGGCTGA
 AL-2b.L 1538 ATATGCATCAGACGACACTGCTCCGGCAACGGGGCCAGTGTGAGGGGCGAA
 AL-2b.L 1588 GCGGGCCAGCATGGTCCCGTGTGATAGGATTGAAGAGGCTACTGAGGAATA
 AL-2b.L 1638 GGGGCGCTTCTCAATGAGAGAGCGCGAGGCTGCTGTTATCATGGGAACCCAGG
 AL-2b.L 1688 CAGATCAATCATCCCTGGCAGGTCAGGGAAGGAAGTTACTTAGCTTCTCCT
 AL-2b.L 1738 TCACCTTCTTCCACAGAAATTTATTATAGGCTTGTTCGAAGTTGTAGTGT
 AL-2b.L 1788 GTGATCAGATTGGTGGTGGCTGTGAGCTCTGTGGTACCTGGCAAGTTCCCG
 AL-2b.L 1838 TCATGGAATTGATATCAAGCTTATCGATACCGTCCACCT (SEQ ID NO: 1)

FIGURE 3B

lerk2 2 MA RFGQRWLGKWL VAMVWVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGG
 huHTKL 1 MAVRRQSYWKYCWGLWV--LCRTAISKSIYLEPIYWNSSVSKFLPGQGG
 AL2.sht 1 MG PPHSGPGGVRYGALLLLQVLGLVSGL--SLEPVYWNSSANKRFOAEGG
 AL2.long 1 MG PPHSGPGGVRYGALLLLQVLGLVSGL--SLEPVYWNSSANKRFOAEGG

lerk2 80 LVLYPKIGDKLDIICPRA--EAGN--PYEYKLYLVLRPEQAAACSTVLQ
 huHTKL 48 LVLYPQIGDKLDIICPKV--DSKTYGQY EYKLYLVVQKQADRCTIKKE
 AL2.sht 48 YVLYPQIGDRLDLLCPRARPPGPHSGPNYEFYKLYLVGGAGRRCEAPPA
 AL2.long 48 YVLYPQIGDRLDLLCPRARPPGPHSGPNYEFYKLYLVGGAGRRCEAPPA

lerk2 95 PNVLVYTCNRPESQIRFTIKFOEFSPNYMGLFQKKNHDDYYITSTNGSLEG
 huHTKL 96 NTPLLNCAKPDQDIKFTIKFOEFSPNLWGLEFQKKNHDDYYIISTNGSLEG
 AL2.sht 96 PNLLLTCDRPLDLRFTIKFOEYSPNLWGHEFRSHHDDYYIATSDGTREG
 AL2.long 96 PNLLLTCDRPLDLRFTIKFOEYSPNLWGHEFRSHHDDYYIATSDGTREG

lerk2 145 LENREGGVCTRTMKIIMKVGCDPNNAVTPQLTTSRPSKEADNTVKMATQ
 huHTKL 146 LDNQEGGVCTRAMKILMKVGQDAAG--AGSTRNKDPTRRPELEAG
 AL2.sht 146 LESLQGGVCLTRGMKVL RVGQSPRGGA VPRKPVSEMPMERDAGAAHSLE
 AL2.long 146 LESLQGGVCLTRGMKVL RVGQSPRGGA VPRKPVSEMPMERDAGAAHSLE

lerk2 195 A PGRGSLQDSQGRHETVNC EKSGPGASGGSSGDPDGF FNGKVALFAAV
 huHTKL 189 YNGRSGSTSPFYKPNQSSSTQNSAGHSQ--NNILGSEVALFAGI
 AL2.sht 190 PGKENLPQDPTSNATSRGAEGPLPPFSMPAVAGAAAGL--ALLLLGVA
 AL2.long 190 PGKENLPQDPTSNATSRGAEGPLPPFSMPAVAGAAAGL--ALLLLGVA

lerk2 245 GAGGVIFLLIIIFLT VLLKLKRRKHTQ-QRAAALSLSLTA SPKGGSG
 huHTKL 232 ASGCIIFIVIIITLV VLLKYRRKRSKSP-GHTTTL SLSLTA TPKRSGN
 AL2.sht 244 GAGGA--MCWRRRRAKPSES RHPGPGSFGRGGS LGLG--GGGMS
 AL2.long 244 GAGGA--MCWRRRRAKPSES RHPGPGSFGRGGS LGLG--GGGMS

lerk2 294 TAGT E P S D I I P L R -- T T E N N Y C P H Y E K V S G C Y G H P V Y I V O E M P P O S P A
 huHTKL 292 N N G S E P S D I I P L R -- T A C S Y F C P H Y E K V S G C Y G H P V Y I V O E M P P O S P A
 AL2.sht 295 P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G C Y G H P V Y I V O D G P P O S P P
 AL2.long 295 P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G O Y G H P V Y I V O D G P P G P P

lerk2 341 N I Y Y
 huHTKL 328 N I Y Y
 AL2.sht 335 N I Y Y
 AL2.long 335 N I Y Y T S I S V L E W P I L H T I Q L P F M R S K C S A V T T F L P P V O V I T T S T O R M T S F

lerk2 345 K V
 huHTKL 332 K V
 AL2.sht 336 K V
 AL2.long 345 S F T T L N P S M O A C R A Q M G E F R I R W C P W G D R I L Q T A L F V L V L I L L G R L N M H

AL2.long 435 Q T T L L R O R A S Y E A E A G O H G P L (SEQ ID NO: 2)

(SEQ ID NO: 9)
 (SEQ ID NO: 10)
 (SEQ ID NO: 4)

FIGURE 4

LERK2.1 1 MA-RPGGRWLQKWL VAMV VWA LCRLATPLAKNLEPVSWSSLNPKFLSGKGG
 huHTKL 1 MAVRRDSVWKYC WGLMV- -LCRTAISKSVLEPIYWNSSNSKFLPGGG
 ALII.long 1 MGPPHSGP-GQVRVGA LLL- -LGV LGLVSGLSLEPVYWNSSANKRFQAEGG

LERK2.1 50 LVIYPKIGDKLDIICPRA- -EAGR- -PYEYKLYLVVRPEQAAAGSTVLD
 huHTKL 48 LVLYPOIGDKLDIICPKV- -DSKTVGQYEYKVMVDKDAQDRCTIKKE
 ALII.long 48 YVLYPOIGDRDL LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPA

LERK2.1 95 PNLVLTG NRPEQEI RFTIKFOEFSPNYMGLFKKKHHDYYITSTNGSLEG
 huHTKL 95 NTPLLNCAKPDODIKFTIKFOEFSPNLWGLEFQKNKDYYIISTNGSLEG
 ALII.long 96 PNL LLTCD RPDLD LRFTIKFOEYSPNLWGHEFRSHHDYYIIATSDGTRREG

LERK2.1 145 LENREGGVCRTRTMKIIMKVGQDPNAVTP EQLTTSRPSKEADNTVKMATO
 huHTKL 145 LDNREGGVCQTRAMKILMKVGQDASS- - -AGSTRNKDPTRRPELEAG
 ALII.long 148 LESLQGGVCLTRG MKVLLRVGQSPR- - -GGA VPRKPVSEMPME- R

LERK2.1 195 APGSRRGSLGDSDGKHETVNQEEKSGPGASGGSSSGDPDGGFFNSKV ALFAAV
 huHTKL 189 TNG-RSSSTTSPPFVKPNPGSSTDGNSAGHSG- - -NNILGSEVALFAGI
 ALII.long 189 DRGA AHSLEPGKENLP GDPTS NATSRGAEG- - -PLPPPSMPAVAGA

LERK2.1 245 GAGCVIFLLIIIFLT VLLKL LRKRHRKHTOORAAALSL- -STLASPKGG
 huHTKL 232 ASGCIIFIVIIITLV VLLKYRRRHRKHSPOHTTTL SL- -STLATPKRS
 ALII.long 232 AGGLALLLLGVAGAGGAMCWRRRRAKPSERHPGPGSFGFRGGSLLGLGGGG

LERK2.1 292 S-GTAGTEPSDIIIPLR- -TTENNYCPHYEKVSGDYGHPVYIVOEMPPO
 huHTKL 279 G-NNNGSEPSDIIIPLR- -TADSVFCPHYEKVSGDYGHPVYIVOEMPPO
 ALII.long 282 GMPREAEPEGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVODGPPPO

LERK2.1 338 SPANIYY- - - - -
 huHTKL 325 SPANIYY- - - - -
 ALII.long 332 SPPNIYYT SISVLEWPILHTIQLFFMRSKCSRVTTLFPVQVITTSTCRM

LERK2.1 345 - - - - -KV- - - - - (SEQ ID NO: 9)
 huHTKL 332 - - - - -KV- - - - - (SEQ ID NO: 10)
 ALII.long 382 TSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRI LGTALFVLVLI LLLGRL

ALII.long 432 NMHQTTL LRORASVEAEAGQHGPL (SEQ ID NO: 2)

FIGURE 5